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EXAMINER

THOMAS, DAVID C

ART UNIT

PAPER NUMBER

1637

NOTIFICATION DATE

DELIVERY MODE

11/18/2008

ELECTRONIC

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

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|                              |                                      |                                     |  |
|------------------------------|--------------------------------------|-------------------------------------|--|
| <b>Office Action Summary</b> | <b>Application No.</b><br>10/583,329 | <b>Applicant(s)</b><br>PALGI ET AL. |  |
|                              | <b>Examiner</b><br>DAVID C. THOMAS   | <b>Art Unit</b><br>1637             |  |

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 23 July 2008.
- 2a) ☐ This action is **FINAL**.                      2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 1-16 is/are pending in the application.
- 4a) Of the above claim(s) 11-14 and 16 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-10 and 15 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All    b) ☐ Some \*    c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
  2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

### Attachment(s)

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)            | 4) <input type="checkbox"/> Interview Summary (PTO-413)           |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)   | Paper No(s)/Mail Date. _____                                      |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date <u>6/16/2006</u> .   | 6) <input type="checkbox"/> Other: _____                          |

## **DETAILED ACTION**

### ***Election/Restrictions***

1. Applicant's election with traverse of Group 1, claims 1-10 and 15 in the reply filed on July 23, 2008 is acknowledged. Claims 11-14 and 16 are withdrawn from further prosecution. Applicant has also elected the following combination of oligonucleotide probe sequences from Group III: SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15 and 17-19. The traversal is on the grounds that Moeckel et al. (U.S. Patent Pub. No. 2003/0166884) does not anticipate or make obvious the subject matter recited in Group I and therefore the inventions listed in Groups I and II relate to a single inventive concept. In particular, Applicant argues that Moeckel does not teach or suggest a method comprising using the DNA primers and probes of claim 1. The Examiner asserts that Moeckel teaches methods of amplification and detection of rpoB gene sequences of a bacterial species using known fragments of the sequenced gene to arrive at suitable primers and probes useful for said amplification and detection (paragraphs 43 and 44 and SEQ ID NO: 1). It would be obvious to design other primers and probes to conserved and hypervariable regions of the rpoB gene to enable detection of different members of the genus *Corynebacterium* based on the disclosed gene sequence of Moeckel. A more detailed method for the detection of infectious bacterial species based on the rpoB gene appears below.

The requirement is still deemed proper and is therefore made FINAL.

***Claim Interpretation***

2. Prior to examination of the claims, the claims must first be construed. In claims 1, 5, 8 and 9, the term “complementary sequences” is used in regard to sequences of primers or probes that comprise specific SEQ ID numbers, “complementary sequences” thereof and/or functional fragments thereof. Since there is no strict definition of “complementary sequences” in the specification, for examination purposes, “complementary sequences” is interpreted as sequences that can hybridize under non-stringent conditions and therefore need not be fully complementary to their target sequences. For prior art purposes, this interpretation is extended to all of the dependent claims of claim 1.

***Claim Rejections - 35 USC § 112***

3. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

4. Claims 1, 4, 5, 10 and 15 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

With regard to claims 1 and 5, primer or probe sequences are said to comprise specific SEQ ID numbers, complementary sequences thereof and/or “functional fragments thereof.” Since there is no strict definition of “functional fragments” in the specification, it is not clear what is claimed by this limitation.

With regard to claim 4, oligonucleotide probe sequences are described as being 15-30, 19-30 or 19-26 nucleic acids in length. Most likely, the term "nucleic acids" meant to read "nucleotides". However, it is also possible the set of oligonucleotide probe sequences contains 15-30, 19-30 or 19-26 nucleic acids. Clarification is required.

Claim 10 recites the limitation "The diagnostic method according to claim 1, wherein the micorarray is used in step c)". There is insufficient antecedent basis for "the microarray technology" in the claim.

Claim 15 provides for the use of the combination of oligonucleotide probes according to claim 14 for the detection, identification, or classification of disease causing bacterial species, but, since the claim does not set forth any steps involved in the method/process, it is unclear what method/process applicant is intending to encompass. A claim is indefinite where it merely recites a use without any active, positive steps delimiting how this use is actually practiced.

Claim 15 is also rejected under 35 U.S.C. 101 because the claimed recitation of a use, without setting forth any steps involved in the process, results in an improper definition of a process, i.e., results in a claim which is not a proper process claim under 35 U.S.C. 101. See for example *Ex parte Dunki*, 153 USPQ 678 (Bd.App. 1967) and *Clinical Products, Ltd. v. Brenner*, 255 F. Supp. 131, 149 USPQ 475 (D.D.C. 1966).

### ***Claim Rejections - 35 USC § 102***

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

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A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

6. Claims 1-10 and 15 are rejected under 35 U.S.C. 102(e) as being anticipated by Drancourt et al. (U.S. Patent Pub. No. 2006/0199182).

Drancourt teaches a diagnostic method for detecting and identifying bacterial species causing infections from a clinical sample (for overview, see Abstract and paragraph 1, lines 1-7; members of the *Streptococcus* genus are responsible for a variety of different infections in man, paragraph 2, lines 19-53), said method comprising:

a) amplifying DNA isolated from said clinical sample using a mixture of DNA primers that comprises sequences which hybridize with the sequences that originate from conserved regions of *rpoB* genes encoding DNA directed RNA polymerase [EC:2.7.7.6] subunit B of bacterial species causing infections (mixtures of degenerate primers are provided that hybridize to consensus sequences of the *rpoB* gene of *Streptococcus* and related genera and are useful as amplification primers, paragraph 29, lines 1-8, paragraph 34, lines 1-5 and paragraph 59, lines 1-7), said sequences comprising SEQ ID NOS: 20 and 21 and/or complementary sequences thereof and/or functional fragments thereof (SEQ ID NOS: 20 and 21 are homologous to nucleotides 359 to 337 and 247 to 265, respectively, of SEQ ID NO:12 of Drancourt representing a fragment of the *rpoB* gene of *Streptococcus pneumoniae*; since no specific hybridization conditions are described, the degenerate primers represented by SEQ ID NOS: 6 and 7

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of Drancourt in paragraph 29 would hybridize under non-stringent conditions to sequences represented by SEQ ID NOS: 20 and 21 or complementary sequences thereof),

b) contacting the amplified DNA with a desired combination of oligonucleotide probe sequences that hybridize under normal hybridization conditions with hyper-variable regions situated near said conserved regions of rpoB genes encoding DNA directed RNA polymerase subunit B of bacterial species causing said infections, said sequences being bacterial species specific under said hybridization conditions (the degenerate primers that hybridize to consensus sequences flank hyper-variable sequences specific to different species of a genus, for which combinations of probes are designed to detect one or more bacterium species in a sample, paragraphs 68 and 69, lines 1-5, paragraph 70, lines 1-6 and paragraph 127, lines 1-9, with each probe of a mixture of probes containing at least 20-30 consecutive nucleotides of the hyper-variable region of its respective species rpoB target, paragraph 96, lines 1-8).

c) detecting the formation of a possible hybridization complex (hybridization of detection probes, which can be labeled with various marking agents, paragraph 21, lines 1-9, with hybridization detected using techniques including dot-blot, Southern or Northern blotting, sandwich techniques or DNA chips, paragraph 98, lines 1-17, paragraph 133, lines 1-8 and paragraph 134, lines 1-5).

With regard to claim 2, Drancourt teaches a diagnostic method wherein said infections causing bacterial species are bacterial species that cause human disease, particularly respiratory tract infections and/or ear, nose and throat diseases (members

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of the *Streptococcus* genus are responsible for a variety of different infections in man, including throat infections and pneumonia, paragraph 2, lines 19-35).

With regard to claim 3, Drancourt teaches a diagnostic method wherein said hyper-variable region is the hyper-variable region of the gene encoding the rpoB protein of a bacterial species selected from *Haemophilus influenzae*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Legionella pneumophila*, *Corynebacterium diphtheriae*, *Mycoplasma pneumoniae*, *Escherichia coli*, *Moraxella catarrhalis* and *Neisseria gonorrhoeae* (the method is based on detection of hyper-variable regions of the rpoB gene of bacterial species, including *Streptococcus pneumoniae* and *Streptococcus pyogenes*, paragraph 69, lines 1-5, paragraph 70, lines 1-6 and paragraph 71, lines 1-9).

With regard to claim 4, Drancourt teaches a diagnostic method wherein the length of oligonucleotide probe sequences used in step b) is 15 - 30, more preferably 19-30, and most preferably 19-26 nucleic acids and are optionally labeled (detection probes used for hybridization assays can be labeled with various marking agents, paragraph 21, lines 1-9, and are preferably 20-30 nucleotides in length, paragraph 96, lines 1-8 and paragraph 97, lines 1-7).

With regard to claim 5, Drancourt teaches a diagnostic method wherein said combination of oligonucleotide probe sequences comprises all or a portion of SEQ ID NOS: 1 to 19, and/or complementary sequences thereof, or functional fragments thereof and preferably it comprises all of the SEQ ID NOS: 1 to 19 (each oligonucleotide probe comprises sequences that include at least 20-30 consecutive nucleotides of the hyper-

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variable region of its respective species *rpoB* target, paragraph 96, lines 1-8; included are probes which can hybridize to SEQ ID NO: 3 or complementary sequences thereof, which is homologous to positions 340-318 of SEQ ID NO: 11 of Drancourt in the *rpoB* gene of *S. pyogenes* and to SEQ ID NO: 5 or complementary sequences thereof, which is homologous to positions 295-274 of SEQ ID NO: 12 of Drancourt in the *rpoB* gene of *S. pneumoniae*).

With regard to claim 6, Drancourt teaches a diagnostic method wherein said combination of oligonucleotide probe sequences is attached onto a solid support, preferably onto treated glass (capture or detection probes may be fixed to solid supports such as microtitration wafers and DNA chips, including those made of glass, paragraph 20, lines 1-5 and paragraph 133, lines 1-5).

With regard to claim 7, Drancourt teaches a diagnostic method wherein the DNA isolated from the clinical sample in step a) is amplified using the polymerase chain reaction (PCR) (amplification of the *rpoB* target sequences is performed by PCR using primers and a DNA polymerase, paragraph 25, lines 1-4 and paragraph 59, lines 1-7) and wherein the DNA amplified in step b) is contacted with the bacterial species-specific oligonucleotide probes attached onto a solid support (target nucleic acids, after PCR amplification, are contacted with probes immobilized on a solid support, paragraph 99, lines 1-2, paragraph 100, lines 1-6 and paragraph 101, lines 1-3).

With regard to claims 8, 9 and 15, Drancourt teaches a diagnostic method wherein suitably labeled nucleotides are used in the amplification of DNA isolated from a clinical sample in step a) to generate a detectable target strand and wherein the

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amplified and optionally labeled target DNA in step b) is contacted with a solid support, preferably treated glass, on which all bacterial species-specific oligonucleotide probes of SEQ ID NOS: 1 to 19 or those shown in Table 3 and/or complementary sequences thereof have been attached (degenerate primers such as SEQ ID NOS: 6 and 7 are used in cycle sequencing reactions, in which dye terminator-labeled nucleotides are used to label the products, paragraph 130, lines 1-7 and paragraph 148, lines 1-8; amplification products, including sequencing products, may be contacted with a DNA chip comprised of glass containing probes corresponding to the hyper-variable regions of the *rpoB* gene of multiple bacterial species, paragraph 20, lines 1-5 and paragraph 133, lines 1-10; each oligonucleotide probe comprises sequences that include at least 20-30 consecutive nucleotides of the hyper-variable region of its respective species *rpoB* target, paragraph 96, lines 1-8; included are probes which can hybridize to SEQ ID NO: 3 or complementary sequences thereof, which is homologous to positions 340-318 of SEQ ID NO: 11 of Drancourt in the *rpoB* gene of *S. pyogenes* and to SEQ ID NO: 5 or complementary sequences thereof, which is homologous to positions 295-274 of SEQ ID NO: 12 of Drancourt in the *rpoB* gene of *S. pneumoniae*; these probes would contain regions that would hybridize to complementary regions of other members of SEQ ID NOS: 1-19 under non-stringent conditions).

With regard to claim 10, Drancourt teaches a diagnostic method wherein the microarray technology is used in step c) (amplification products, including sequencing products, may be contacted with a DNA chip containing probes corresponding to the

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hyper-variable regions of the rpoB gene, paragraph 20, lines 1-5 and paragraph 133, lines 1-10).

### ***Conclusion***

7. Claims 1-10 and 15 are rejected. No claims are allowable.

### ***Correspondence***

8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to David C. Thomas whose telephone number is 571-272-3320 and whose fax number is 571-273-3320. The examiner can normally be reached on 5 days, 9-5:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/David C Thomas/

Examiner, Art Unit 1637

/Kenneth R Horlick/

Primary Examiner, Art Unit 1637